AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior versions, and listings, of claims in the application.

1.-41. (Cancelled)

42. (Currently Amended) A method for the detection of *L. brevis* in a sample, which comprises the following steps:

(a) bringing the sample into contact with a combination of at least two first nucleic acid molecules (primers), which hybridize with a region of a *L. brevis* nucleic acid, wherein each of the at least two first nucleic acid molecules ~~are~~ is selected from the group consisting of:

(i) ~~a nucleic acid sequence consisting of~~ SEQ ID NO 1, 21, 73 or 74, or a fragment thereof of ~~comprising at least~~ 15 to 30 ~~10~~ nucleotides,

(ii) a nucleic acid which specifically hybridizes under stringent conditions with SEQ ID NO: 1, 21, 73, or 74, wherein the stringent conditions comprise hybridizing the nucleic acids at 50 °C with a hybridization solution consisting of 2.5X SSC, 2X Denhardts solution, 10 mM TRIS, 1 mM EDTA pH 7.5, and 1 minute washings in 0.1 X SSC to 1.0 X SSC, 2X Denhardts solution, 10 mM TRIS, 1mM EDTA pH 7.5 at 20-50 °C repeated four times, and ~~with a nucleic acid according to (i),~~

~~(iii) a nucleic acid which is at least 70% identical with a nucleic acid according to (i) or (ii), and~~

(iii) ~~(iv)~~ a nucleic acid which is complementary to a nucleic acid according to (i) and (ii) ~~(iii)~~,

(b) amplifying the *L. brevis* nucleic acid or a portion thereof to produce at least one amplification fragment;

(c) contacting the amplification fragments obtained in step (b) with at least one second nucleic acid molecule (probe), which specifically hybridizes with at least one amplification fragment that comprises a sequence of the microbial nucleic acid specific for *L. brevis*, wherein the at least one second nucleic acid molecule is selected from the group consisting of:

(i) ~~a nucleic acid sequence consisting of~~ SEQ ID NO: 21, 73 or 74, or a fragment thereof of ~~comprising at least~~ 15 to 30 ~~10~~ nucleotides,

(ii) a nucleic acid of (i) which is modified such that one or two nucleotides in 10 consecutive nucleotides of (i) are replaced by nucleotides which do not naturally occur in bacteria ~~which specifically hybridizes with a nucleic acid according to (i),~~

~~(iii) a nucleic acid which is at least 70% identical with a nucleic acid according to (i) or (ii), and~~

(iii) ~~(iv)~~ a nucleic acid which is complementary to a nucleic acid according to (i) or (ii)-~~(iii),~~ and

(d) detecting at least one hybrid nucleic acid which consists of an amplification fragment and a second nucleic acid molecule introduced in step (c), whereupon *L. brevis* is detected in a sample.

43.-49. (Cancelled)

50. (Previously Presented) The method according to Claim 42, characterized in that the amplification comprises a polymerase chain reaction (PCR).

51. (Previously Presented) The method according to Claim 42, characterized in that the amplification comprises a ligase chain reaction.

52. (Previously Presented) The method according to Claim 42, characterized in that the amplification comprises an isothermal nucleic acid amplification.

53. (Previously Presented) The method according to Claim 42, characterized in that the second nucleic acid molecule is modified or labeled to produce a detectable signal, wherein the modification or label is selected from the group consisting of (i) radioactive groups, (ii) colored groups, (iii) fluorescent groups, (iv) groups for immobilization on a solid phase and (v) groups which allow an indirect or direct reaction by means of antibodies, antigens, enzymes and/or substances with affinity for enzymes or enzyme complexes.

54.-64. (Cancelled)